

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 15, 2003, 03:45:56 ; Search time 2149 Seconds
(without alignments)
3751.269 Million cell updates/sec

Title: US-09-600-932-2

Perfect score: 1484
Sequence: 1 NMGFASLRRNQFILLVFL.....NDTECHLIMYFVCEIKKK 277

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-Q/cgn2.1/USPTO.spool/US09600932.r/unat.09062003.094530.25981/app.query.fasta_1.455
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-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdt -LIST=45
-DOCLIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-USER=US09600932.cgn2.1.1652-@runat.09062003.094530.25981 -NCPD=6 -ICPD=3
-NO_MMAP -LARGEDEV -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
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33: em_htg_mus:*
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35: em_htg_rod:*
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37: em_htg_vrt:*
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39: em_htgo_hum:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1484	100.0	1594	AB002631	AB002631 Homo sapi
2	1484	100.0	1595	E29008	E29008 Novel colle
3	1472	99.2	1016	AX376032	AX376032 Sequence
4	720.5	48.6	141262	AC080033	AC080033 Homo sapi
5	720.5	48.6	182475	AC023487	AC023487 Homo sapi
6	719.5	48.5	1238	AX403469	AX403469 Sequence
7	719.5	48.5	1238	AX454582	AX454582 Sequence
8	719.5	48.5	1238	AX491060	AX491060 Sequence
9	719.5	48.5	1257	BC000078	BC000078 Homo sapi
10	682	46.0	267118	AC097055	AC097055 Rattus no
11	673	45.4	167718	AC115924	AC115924 Mus muscu
12	459	30.9	139357	AC010907	AC010907 Homo sapi
13	351	23.7	1310	AY071821	AY071821 Bos tauri
14	349.5	23.6	1454	BTLSPD	BTLSPD
15	344.5	23.2	1183	BC003705	BC003705 Mus muscu
16	344.5	23.2	1253	MUSSPD	MUSSPD
17	344	23.2	1095	BTCA3	BTCA3
18	338.5	22.8	1385	AF132496	AF132496 Sus scrof
19	337	22.7	1410	AX334792	AX334792 Sequence
20	337	22.7	1410	HSNRPD	HSNRPD
21	337	22.7	1559	AF231714	AF231714 Gallus ga
22	334.5	22.5	1000	AF227738	AF227738 Danio rer
23	333	22.4	1265	RATSPD	RATSPD
24	333	22.4	1301	BC022318	BC022318 Homo sapi
25	332.5	22.4	1305	BTCONGL	BTCONGL
26	330.5	22.3	1284	AF509590	AF509590 Bos tauri
27	328.5	22.1	1385	BOVCGT	BOVCGT
28	328.5	22.1	1392	E16477	E16477 Artificial
29	328.5	22.1	1519	BOVCOGLUTA	BOVCOGLUTA
30	327.5	22.1	714	AF022226	AF022226 Gallus ga
31	327.5	22.1	714	AR182170	AR182170 Sequence
32	316	21.3	1054	AF227737	AF227737 Cyprinus
33	307	20.7	934	AF227739	AF227739 Carassius
34	305.5	20.6	2967	RABSPARO	RABSPARO
35	298	20.1	1052	AF211856	AF211856 Ovis arie
36	298	20.1	1901	AF076633	AF076633 Ovis arie
37	297.5	20.0	805	MACMBPC	MACMBPC
38	294	19.8	888	AB015963	AB015963 Equus cab
39	293.5	19.8	1010	E37364	E37364 Swine serum
40	291	19.6	799	MACBAPA	MACBAPA
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42	290	19.5	1098	BC010760	BC010760 Mus muscu
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45	289.5	19.5	900	AR182149	AR182149 Sequence

RESULT 1

ALIGNMENTS

AB002631
LOCUS AB002631 1594 bp mRNA linear PRI 24-JUN-1999
DEFINITION Homo sapiens mRNA for collectin 34, complete cds.
ACCESSION AB002631.1 GI:5162874
VERSION AB002631.1
KEYWORDS collectin 34.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Ohtani, K., Suzuki, Y., Eda, S., Kawai, T., Kase, T., Yamazaki, H.,
1 (sites)
Ohtani, K., Sakai, Y., Fukuchi, A., Sakamoto, T. and Wakamiya, N.,
Keshi, H., Molecular cloning of a novel human collectin from liver (CL-L1)
J. Biol. Chem. 274 (19), 13681-13689 (1999)
MEDLINE 99240768
REFERENCE 2 (bases 1 to 1594)
AUTHORS Ohtani, K.
TITLE Direct Submission
JOURNAL Submitted (04-APR-1997) Katsuki Ohtani, Osaka Prefectural Institute
of Public Health, Department of Pathology, 3-69, Nakamichi 1-chome
Higashinari-ku, Osaka, Osaka 537, Japan
(E-mail: suzuki@iph.pref.osaka.jp, Tel: +81-6-972-1321,
Fax: +81-6-972-0772)
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ORIGIN
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Score: 1484.00 Matches: 277
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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QY 21 LeuGlnIleGlnSerLeuGlyLeuAspIleAspSerArgProThrAlaGluValCysAla 40
DB 66 TTGCAAAATTCAGAGTCTGGGCTCGATATGATAGCCGCTCCTACCGCTGAAGTCTGTGCC 125
QY 41 ThrHisThrIleSerProGlyProGlyAspAspGlyGluysGlyAspProGlyGlu 60
DB 126 ACACACCAATTTTACCCAGACCCCAAGAGATGATGTAAGAAAGAGATCCAGAGAA 185
QY 61 GluGlyLysHisGlyLysValGlyArgMetGlyProGlyGlyIleLysGlyGluLeuGly 80
DB 186 GAGGAGAAAGCATGGCAAGTGGGACGATGGGCGCAAGAAAGTAAGCAAGCACTGGCT 245
QY 81 AspMetGlyAspArgGlyAsnIleGlyLysThrGlyProIleGlyLysGlyAspLys 100
DB 246 GATATGGAGATCGGGCAATATTGGCAAGACTGGCCCAATTTGGGAGAAAGGCTGACAA 305

QY 101 GlyIleLysGlyLeuLeuGlyIleProGlyGlyLysGlyLysAlaGlyThrValCysAsp 120
DB 306 GGGGAAAAAGGTTTGGCTTGGATACCTCGAGAAAAAGCAAGCAAGGATGCTGTGGAT 365
QY 121 CysGlyArgGlyArgGlyPheValGlyIleLeuAspIleSerIleAlaGlyLeuThr 140
DB 366 TGTGGAAGATACCGGAAATTTGGAGCAACCTGATATATATGTCGCCGCTCAAGACA 425
QY 141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGlyThrGluLysPheThr 160
DB 426 TCTATGAAGTTTGCAGAAAGTATGATACGAGGATTTGGGAAACTGAAAGAAATTTTAC 485
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QY 201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGluArgGlyGlnTyr 220
DB 606 AAGATGGCTCTTCTCGGGTGTTCATTTGGGTGATGACCTTGAAAGGAGGACACTAC 665
QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTyrAsnGluGlyProSer 240
DB 666 ATGTTTCACAGCAACACTCCACTCAGAACTATAGCAACTGAGATGAGGGGAAACCCAGC 725
QY 241 AspProTyrGlyHisGluAspCysValGluMetLeuSerSerGlyArgTyrPasnAspThr 260
DB 726 GACCCCTATGCTCATGAGAGCTGTGTGAGATGCTGTGCAATGAGAAATGACACA 785
QY 261 GluCysHisLeuThrMetTyrPheValCysGluPheIleLysLysLysLys 277
DB 786 GAGTGCATCTTACCATGATCTTGTCTGTGAGTTCATCAAGAGAAAG 836
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LOCUS E29008 1595 bp DNA linear PAT 18-JUN-2001
DEFINITION Novel collectin.
ACCESSION E29008
VERSION E29008.1 GI:13018416
KEYWORDS JP 1999206377-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Nobutaka, W.
TITLE Novel collectin
JOURNAL Patent: JP 1999206377-A 1 03-AUG-1999;
FUSO YAKUHIN KOGYO KK
OS Homo sapiens (human)
PN JP 1999206377-A/1
PD 03-AUG-1999
PF 23-JAN-1998 JP 1998011281
PR NOBUTAKA WAKAMIYA
PC C12N15/09, C07K14/47, C07K14/78, C12P21/00, C12N15/00 CC
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CC Topology: Linear;
FH key Location/Qualifiers
FT CDS location/Qualifiers
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Pred. No.: 2,78e-115 Length: 1595
Score: 1484.00 Matches: 277

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 742 GACCCTATGATGTCATGAGACTGTCGAGATGCTGTCGACATGCAATGACACA 801
Db 261 GluGlyHisLeuMetTyrPheValCysGluPheLeuLysLysLys 277
 802 GAGTGCATCTTACCATGATCTGTCTGTGAGTTCATCAAGAAAGAAAG 852
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LOCUS Homo sapiens chromosome 8, clone RP11-885J16, complete sequence.
DEFINITION AC080033
ACCESSION AC080033.10 GI:18767530
VERSION HTG.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 141262)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 8, clone RP11-885J16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 141262)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barna, N., Bastien, V., Bede, F., Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G., Campolano, A., Castle, A., Choepel, Y., Collangelo, M., Collins, S., Collymore, A., Cooke, P., Deatrelano, K., Dewar, K., Diaz, J. S., Dodge, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Iliev, I., Johnson, R., Jones, C., Kahn, L., Karatas, A., Lacombe, K., Lamares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., Liu, G., MacDonald, P., Margulis, N., McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spengler, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
JOURNAL Direct Submission
REFERENCE Submitted (23-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 141262)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campolano, A., Chang, J., Chazaro, B., Choepel, Y., Collangelo, M., Collins, S., Collymore, A., Cooke, A., Cooke, P., Deatrelano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Huime, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacombe, K., Lamares, R., MacDonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Morrow, J., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2002) Whitehead Institute/MIT Center for Genome

REFERENCE 4 (bases 1 to 141262)
AUTHORS Research, 320 Charles Street, Cambridge, MA 02141, USA
 Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campolano, A., Chang, J., Chazaro, B., Choepel, Y., Collangelo, M., Collins, S., Collymore, A., Cooke, A., Cooke, P., Deatrelano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Huime, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacombe, K., Lamares, R., MacDonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Morrow, J., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT All repeats were identified using RepeatMasker:
 Smt, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center code: RIBR
 Center: Whitehead Institute/ MIT Center for Genome Research
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: LI0939
 Center clone name: 885_J_16

FEATURES
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                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE         Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS           1 (bases 1 to 182475)
                  Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
FEDERSPIEL,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Komp,C., Kottler,S., Lam,B., Marache,R., Miranda,M.,
Morehouse,A.J., Nguyen,M., Oefner,P., Palm,C.J., Ramirez,D.,
Southwick,A.M., Webb,C., Wilhelmy,T., Yu,S. and Davis,R.W.
JOURNAL           2 (bases 1 to 182475)
REFERENCE         Bruno,D., Conn.L., Dela Rosa,M., Faulkner,D., Federspiel,N.,
AUTHORS           Glukhov,S., Hansen,N., Hyman,R., Mao,J., Marathe,R.,
MOREHOUSE,A.J., Oefner,P., Palm,C.J., Ramirez,D.,
YU,S. AND DAVID,R.W.
TITLE             Direct Submission
JOURNAL           Submitted (14-FEB-2000) DNA Sequencing and Technology Center,
SOURCE            Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
COMMENT           On Mar 16, 2001 this sequence version replaced gi:1332478.
                  ----- Genome Center
Center: Stanford DNA Sequencing and Technology Development
Center
Center code: SDSRDC
Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu
                  ----- Project Information
Center project name: 844
Center clone name: RP11-164H21
                  ----- Summary Statistics
Sequencing Vector: M13mp18; X02513; 98% of reads
Sequencing Vector: plasmid; plasmid.accession; 2% of reads
Chemistry: Dye-primer; 0% of reads
Chemistry: Dye-terminator Big dye; 99% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 180260 bases at least Q40
Consensus quality: 180441 bases at least Q30
Consensus quality: 180507 bases at least Q20
Insert size: 178614; agarose-fp
Insert size: 182275; sum-of-contigs
Quality coverage: 8.1x in Q20 bases; agarose-fp
Quality coverage: 7.9x in Q20 bases; sum-of-contigs.
* NOTE: This is a working draft sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* *
* 1      42072: contig of 42072 bp in length
*        42073      42172: gap of unknown length
*        42173      109254: contig of 67082 bp in length
*        109255      109355: gap of unknown length
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BASE COUNT	56447 a	33954 c	34262 g	57610 t	202 others
ORIGIN					
Alignment Scores:					
Pred. No.:	6.38e-49	Length:	182475		
Score:	720.50	Matches:	158		
Percent Similarity:	56.15%	Conservative:	11		
Best Local Similarity:	52.49%	Mismatches:	39		
Query Match:	48.55%	Indels:	93		
Db:	2	Gaps:	6		
US-09-600-932-2 (1-277) x AC023487 (1-182475)					
Qy	66	LysValaGlyArgMetGlyProIyGlyIleLysGlyGluLeuGlyAspMetGlyAspArg	85		
Db	6734	AAACTCGGGAAGAGTACTGCCATGTCTATCCAGAGGCAFTTGGAAAGACTTC-----	6684		
Qy	86	GlyAsnIleGlyLysThrGlyProIleGlyLysIyGlyAspLys-----Gly	101		
Db	6683	---TTATAGGAGGAAATATTTCCACTGATCTTAAGAGGATGATGAGAAAGTTTACAGGT	6627		
Qy	102	GluIySGlyLeuLeuGlyIleProGlyGluIySGlyLysAlaGlyThValCysAspCys	121		
Db	6626	AGAAAGACTTTCATGGCATAAAGGCTTGGAAAGTAAAGAAAAGGCGCTGCATGT	6567		
Qy	121	-----	121		
Db	6566	AGCCACAGTATAGCTAAAGCATAAAGTATGTTGGAAATATATGATGATGGGCTGCG	6507		
Qy	121	-----	121		
Db	6506	TGAAAGTTCAATGTAACATGCTCTTGTCTCAACTTGTGCTGCCAGGTGTGAGAAATTGA	6447		
Qy	122	-----GlyArgThyArgLysPheValGlyIleuAspIle	133		
Db	6446	GGAGAAAAGAAAGGAGAAACAAAGGTATGATGTCTCTATTGTCTACTAGAGGTG	6387		
Qy	134	SerIlealaArg-----	137		
Db	6386	GGGGTAAATTAATCTGTGACTACTCTCATTAATAGGCGCTTGAATAATATTTGTGAATAT	6327		
Qy	138	-----LeuLysThrSerMetLysPheVal-----	145		
Db	6326	GAATTAATTAATGTAATCTGTGCAATATCATATATTTTGTGCTTATCTTTTGAG	6267		
Qy	146	---LysAsn-----ValIlealaGlyIleArgGluThrGlu	156		
Db	6266	ATAGCTATGATACTCTCTTTTCTCTCCCTCAGTATGAGGATTAAGGAAATGAAACATGA	6207		
Qy	157	GluIySPheTyrrTyIleValGlnGluGluLysAsnTyrrArgGluSerLeuThrHisCys	176		
Db	6206	GAGAAATTCATCTCATCTGTGACAGAGAGAAATCAACAGGAAATCCCTTAACCCATGCG	6147		
Qy	177	ArgIleArgGlyGlyMetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIleAla	196		
Db	6146	AGAGTTGGGGTGGAAATGCTAGCCATGCGCCAGAGATGAAGCTGCCAACACATCTAGCT	6087		
Qy	197	AspTyrrAlaAlaLysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGluArg	216		
Db	6086	GACTATGTGTGCCAAGAGTGGCTTCTTTCGGGTGTTCATGTGCGTGAATGACCTTGAAGG	6027		
Qy	217	GluIyGlnTyrrMetPheThrAspAsnThrProLeuGlnAsnTyrrSerAsnThrAspGlu	236		
Db	6026	GAGGAGACATCATGTTTCCACAGAACACTCTCAGCAATATAGCACTGGAAATGAG	5967		
Qy	237	GlyIleuProSerAspProTyrrGlyHisGluAspCysValGluMetLeuSerSerGlyArg	256		
Db	5966	GGGGAACCCAGCAGCCCTATGATGATGAGAGACTGTGAGATGATGAGCTTGCGGAGA	5907		
Qy	257	TrpAsnAspThrGluCysHisLeuThrMetTyrrPheValCysGluPheIleLysLysLys	276		
Db	5906	TGGATATGACACAGAGTGCATCTTAACATGTACTTTGTCTGTGATTCATCAACAAAGAA	5847		

LOCUS	AX403469	1238 bp	DNA	linear	PAT 14-JUN-2002
RESULT 6	AX403469				
DEFINITION	Sequence 356 from Patent WO0073454.				
ACCESSION	AX403469				
VERSION	AX403469.1	GI:21436970			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnovers, L., Eaton, D., Ferrara, N., Gerber, H., Gertlesen, M., Goddard, A., Godowski, P., Grimaldi, C.J., Gurney, A.L., Kijavlin, I., Napier, M.A., Pan, J., Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K., Williams, P., Wood, W.I. and Zhang, Z.				
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same				
JOURNAL	Patent: WO 0073454-A 356 07-DEC-2000;				
FEATURES	Genetech Inc. (US)				
SOURCE	Location/Qualifiers				
BASE COUNT	293 a 321 c 389 g 235 t				
ORIGIN					
Alignment Scores:					
Pred. NO.:	2.13e-51	Length:	1238		
Score:	719.50	Matches:	130		
Percent Similarity:	67.74%	Conservative:	59		
Best Local Similarity:	46.59%	Mismatches:	81		
Query Match:	48.48%	Indels:	9		
DB:	6	Gaps:	3		
US-09-600-932-2 (1-277) x AX403469 (1-1238)					
OY	3 GlypheaLaserLeuLeuArgArgAsnInHeLeuValLeuPheLeuGln 22				
DB	46 GGTGTCCTCGCTCGCGCTCAGATGAGGGGGAATCTGGCCCTGGTGCGCTTAAATCAGC 105				
OY	23 ILeGInserLeuGlyLeuAspLLeaSpSerArgProThraL-----GlyValCys 39				
DB	106 CTGGCCCTTCCTGTCACCTCTGCCATCTGCACATCTCAGCCGGCTGGCGATGACCGCTTC 165				
OY	40 AlaThrHisThrIleSerProGlyProLysGlyAspAspGlyGluLysGlyAspProGly 59				
DB	166 TCTGTGCAGATCCGTCGCTCGCCCTCAAGAGGGATGCGGGAGAGAGAGAGC----- 219				
OY	60 GluGluGlyLysHisGlyLysValGlyArgMetGlyProLysGlyIleLysGlyLeu 79				
DB	220 ---AAAGCGCCGCCCGGACGCGCTGGAAGATCGGCCCGCCAGGAGAAAAGAGACATG 276				
OY	80 GlyAspMetGlyAspArgGlyAsnLe-----GlyLysThrGlyProIleLeuLys 96				
DB	277 GGGGCAAAAGACAGAAAGGCAAGTGTGGCTGCTCATGGAATAATGTGCTCCATTGGCTCT 336				
OY	97 LysGlyAspLysGlyGluLysGlyLeuLeuGlyIleProGlyGluLysGlyLysAlaGly 116				
DB	337 AAAAGTGAAGAAAGGATTCGCGGACATATAGAACCCCGTGGTCCATATGAGAACACAGGC 396				
OY	117 ThrValCysAspCysGlyArgTyrArgLysPheValGlyGluLeuAspLLeSerIleAla 136				
DB	397 CTCCCATGTGTGTCAGCCACCTCGCGCAAGCCATCGGGGAGATGAGAACACAGGTCTCT 456				
OY	137 ArgLeuLysThrSerMetLysPheValLysAsnValIleAlaGlyIleArgGluThrGlu 156				
DB	457 CAGCTGACACGACGACCTCAAGTTCATCAAGATGTCTGTGCGCGGTGTGGCGACAGCGAG 516				

OY		157	GLUysrhefyrTTLvlealGlnluyasnrYrArgusierLeuthNisCys	176
Dd		517	AGCAAGATCTACCGTCGTGGTAGAGAGAGAAGGCCGTACGGCGAGCCACTCTCTGC	576
OY		177	ArGlleaRgglgylmEtleLualmeProlbsAspgJualaaLaanThrlEuIllea	196
Dd		577	CAGGGCGGGGGCACGCTGAGCATGCCAACGAAGACAGGGGTGGCAATTGGCTATGGCC	636
OY		197	AspyrrTaLaAlalySserglYpherpheArYaItheileglYValaasnspPleunrg	216
Dd		637	GCAATACCTGGGCGAAGCGGGCGCTGGCCCGTGCTCTTCATCGGCACAACAGCACTGGAANAAG	696
OY		217	GlUlglYglInrymEtPheThlrAspnAnThrpProeugLnAsnYrSerAsnTrlpAsnglu	236
Dd		697	GAGGGCCCCCTTCGCTACTCTGACCACTCCGCCCATCGGGACCTTCAACAACTGGCGCACG	756
OY		237	gLyglubProserApPrOtyrGlyHiegluaSpCySaIgUmEtleUsenSerGlyArq	256
Dd		757	GGTAGGCCCAACAATGCTTACGACGAGAGAGAGACTGCGAGATGGTGGCTCGGGCGGC	816
OY		257	TrrpsnaRprThrgLucYshIsLeuthMethyrrpHevalCysglUpheilleYlys	275
Dd		817	TGGACAGACGTGGCGCTCCACACCACCACTGACTTCAATGtGTGATTGACCAAGAG	873
RESULT 7				
AX454582				
LOCUS	AX454582	1238 bp	DNA	linear PAT 06-JUL-2002
DEFINITION	Sequence 167 from Patent WO0208284.			
VERSION	AX454582			
KEYWORDS	AX454582.1 GI:21713915			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homniidae; Homo. Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Pooni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W. Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis Patent: WO 0208284-A 167 31-JAN-2002; Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone (US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard, Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US); Hillan, Kenneth J. (US); Marsters, Scott A. (US); Pan, James (US) ; Paoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William I. (US)			
TITLE	Location/Qualifiers			
JOURNAL	source			
BASE COUNT	293 a 321 c 389 g 235 t			
ORIGIN	/organism:"Homo sapiens" /db_xref="taxon:9606"			
Alignment Scores:				
Pred. NO.:	2.13e-51	Length:	1238	
Score:	719.50	Matches:	130	
Percent Similarity:	67.74%	Conservative:	59	
Best local Similarity:	46.59%	Mismatches:	81	
Query Match:	48.48%	Indels:	9	
DB:	6	Gaps:	3	
US-09-600-932-2 (1-277) x AX454582 (1-1238)				
OY		3	glybehaLaserleuearGargAnsclnPhelleureuValleuPheuleuGln	22
Dd		46	GGTCTCCTCGCTGGCGCTCAGAGATAGGGGCAATCTGGCCCTGTGGCGGCTTTATACAC	105
OY		23	IleclnserieuGlYleuasPlleAspseraGrProthrAla-----gluValcys	39

Db		106	CTGGCGCTTCGTTACATAGCTGCCATTCTGCATCTCAGCCGGGTGGCGATGACGCTGC	165
OY		40	AlathrhsthrllieserproglyProlysglyasparglygylaspprogly	59
Db		166	TCTGTGCAGATCCTCGTCCCGGCTCAAAAGGATGGGAGAAGGGGAGAC-----	219
OY		60	gluglglgylshisaglyvalglIArgmetglyProlysglylleysglyleu	79
Db		220	---AAAGCGCCCCCGACGGCCCTGGGAAGATCGGGCCCACGGAGAAAAAGGACATG	276
OY		80	GlyaspmetglyasparglyAsnile-----glystrhglyproileglyLys	96
Db		277	GGGGACAAGGACGAAAGGACGATGGTGTCATGCAAAAATTGGTCATGGCTCT	336
OY		97	Lysglaspaplysglygyluleumenglylleproglygylusglylyala gly	116
Db		337	AAAGGTGAAAGAGATCCGGTAGACTTAGAGCCCCGTGCTTAATGGGAACAGGC	396
OY		117	ThryalcyaspCysglyarglyArglyspheValglyleuAspIleserlleala	136
Db		397	CTCCCATGTAGTCAGACGACCTCGCAAGGCCATCGGGAGATGAGAACAGGTCTCT	456
OY		137	ArgleuwsthrsermetlyspheVallysasnValleahaglylleahrglu	156
Db		457	CAGCTGACCAGCAGCTCAAGTTATCAAGAAATCTGTGGCGGTGGCGGAACGAG	516
OY		157	GluyaspheTyrryleValIgngluglulysAsntyArggJguSerleuthIsCys	176
Db		517	AGCAAAGNTCACTCGCTGAGGAGAGAGAAAGCGCTAAGCGGACGCCAGCTTCCTGC	576
OY		177	ArglleatrgglygmelleualmeProlysaspgluaialaasnThrleullea	196
Db		577	CAGGCGCGCGGGGACGCTGAGATGCCCAAGACGAGCGCTGCCAATGGCTATGGCC	636
OY		197	AspyrValAlatysserglyPhepheArgyallelglylaasnaspLeuGluArg	216
Db		637	GCATACCTGGGCGCAAGCGCGCTGGCCCGTCTTCACTGGCATCAACAGACTGGAGAG	696
OY		217	GluclyglnTyrmethPheThrAspAsnthrProleuglnAsnyrSeraThrAsnGlu	236
Db		697	GAGGCGCGCTTCGTACTGTGACCACTCCCGCATGGGAGACTTCAACAATGGCGGAGC	756
OY		237	GlygluPProsearPProtyrGlyHiegluaspCyValGimelleuserSerglyArg	256
Db		757	GGTAGGCCCAACAATGCCCTACGACGAGAGAGACTCGTGAGATGGTGGCTCGGGCGGC	816
OY		257	TrpAsnapthrngLucySHisLeuthrMetlyrPheValCysgluIpheilleLys	275
Db		817	TGGAACGACGTGGCGCTGCACACCAACCATGTACTCATGTGTGAGTTGACAAAGAG	873
RESULT 8				
LOCUS	AX491060	1238 bp	DNA	linear PAT 16-NOV-2002
DEFINITION	Sequence 167 from Patent WO0200690.			
VERSION	AX491060			
KEYWORDS	AX491060.1 GI:22323867			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
	1 Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,			
	Godwin,R.P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,			
	Pooni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.			
	and Ye,W.			
TITLE	Compositions and methods for the diagnosis and treatment of			
JOURNAL	disorders involving angiotensin			
	Patent: WO 0200690-A 167 03-JAN-2002;			
FEATURES	Genentech, Inc. (US)			
SOURCE	Location/Qualifiers			
	I..1238			

BASE COUNT		293 a		321 c		389 g		235 t	
ORIGIN									
Alignment Scores:									
Prid. No.:		2,13e-51		Length:		1238			
Score:		719.50		Matches:		130			
Percent Similarity:		67.74%		Conservative:		59			
Best Local Similarity:		46.59%		Mismatches:		81			
Query Match:		48.48%		Indels:		9			
DB:		6		Gaps:		3			
US-09-600-932-2 (1-277) x AX491060 (1-1238)									
OY	3	GlyPheAlaSerLeuLeuAlaGTAAGTAAGnGlnPheIleLeuLeuValLeuPheLeuLeuGln	22						
Db	46	GGTGTCTCTGGCTGGCTGCAGGATGAGGGGGAAATCTGAGCCCTGTGTGGCTTTAAATCAAC	10						
OY	23	IlleGlnSerLeuGlyLeuAlaPheIleAspArgProThrAla-----GluValCys	39						
Db	106	CTGGCCCTTCTGTACACGTGCGCATCTGCAGATCCTCAACCGGCTGGCATATACGCTTC	16						
OY	40	AlaThrHisThrIleSerProGlyProGlyGlyAspAspGlyGluGlySerProGly	59						
Db	166	TCTGTGCAGATTCCTCGTCTGCTGCCTCAAAAGGGGATGCGGAGAGAAAGAGAGAC-----	21						
OY	60	GluGluGlyLeuGlyHisGlyLeuValGlyArgMetGlyProGlyGlyIleLeuGlyGluLeu	79						
Db	220	---AAAGCGCCCGCCGAGCGCCCTGGAAAGTGTGGCCCCACGGAGAGAAAAGAGACATG	27						
OY	80	GlyAspMetGlyAspArgGlyAsnIle-----GlyLeuThrGlyProIleGlyLeu	96						
Db	277	GGGCAACAAGACAGAAAGACAGTGTGGCTCATGAGAAATTTGGTCCATTGGCTCT	33						
OY	97	LeuGlyAspLeuGlyGlyGlyLeuLeuGlyIleProGlyGluGlyGlyLeuGlyLeuGly	11						
Db	337	AAAGGTAGAAAGAGATTCCTCGGTGACATATGGACCCCTGTGTCTTAATGAGAACAGGC	39						
OY	117	ThrValCysAspCysGlyArgTyrArgLeuPheValGlyIleLeuAspIleSerIleAla	13						
Db	397	CTCCCATGTAGTACACACCAGCTGCGCAAGGCATCGGGGAGATGACAAACAGGTCTCT	45						
OY	137	ArgLeuLeuThrSerMetLeuPheValLeuAsnValIleAlaGlyIleArgGluThrGlu	15						
Db	457	CAGGTGACCAAGCAGCTCAAGTTCATCAAGAAATGCTGTGCCGTGTGGCAGAGAGAG	51						
OY	157	GluLeuPheTyrTrpIleValGlnGlnGluLeuAsnTyrArgGlySerLeuThrHisCys	17						
Db	517	AGCAAGATCTACCTGCTGTGTGAAGAGAGAAACGCTACGCGGAGCCCAACGATGCTCTC	57						
OY	177	ArgIleArgGlyGlyMetLeuAlaMetProGlyAspGluAlaAlaAsnThrIleuIleAla	19						
Db	577	CAGGCGCGGGGGGACAGCTGACATATGCCCAAGAGAGAGCTCCCAATGGCTGTGAAGGCC	63						
OY	197	AspTyrValAlaLeuSerGlyPhePheArgValPheIleGlyValAsnAspLeuGlnArg	21						
Db	637	GCATACCTGGCGCAAGCGCGCCCTGGCCCGTGTTCATCGGCATCAACGACTCGAGAGAG	69						
OY	217	GluGlyGlnTyrMetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTrpAsnGlu	23						
Db	697	GAGGGCGCCCTTGTGTACTGTGACCACTCCCCCATCGGAGACCTTCAACAAAGTGGCGACAG	75						
OY	237	GlyGluProSerAspProTyrGlyLeuHisGlyAspCysValGluMetLeuSerSerGlyArg	25						
Db	757	GGTAGGCCCAACAATGCTTACGACGAGAGAGAGACTGTGTGAAGTGTGTGGCTTCGGCGGC	81						
OY	257	TrpAsnAspThrGluCysHisIleuThrMetTyrPheValCysGluPheIleLeuGly	27						
Db	817	TGGAACGACGCTGGCGCTGCCACACCACCATGTACTTATGTGTGTGATTGACAAAGAGAG	83						

Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Eamhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlik, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Homs, F., Howard, S., Huber, J., Hui, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kuresh, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, Z., Licharge, O., Lie, C., Liu, J., Liu, R., Louisse, H.,
Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapa, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mathew, E., McLeod, M.P., Meador, M., Mel, G., Metzger, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, A., Nguyen, N.,
Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okunolu, G.,
Oragunye, N., Oyedero, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rivers, M., Rojas, A., Rojubo, I., Rolfe, M., Ruiz, S., Savary, G.,
Scherer, S., Scott, G., Shen, H., Shoshitari, N., Sisson, I.,
Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Swatek, A., Tabor, P., Tameris, A., Tameris, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, F., Telford, B., Thomas, N., Thomas, S.,
Uman, K., Vasquez, L., Vera, V., Villalobos, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S.,
Williams, G., Williamson, A., Wlezyk, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G., and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 267118)
Worley, K.C.

Direct Submission
Submitted (06-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 267118)

Direct Submission
Submitted (31-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 24, 2002 this sequence version replaced g1:17063112.

----- Genome Center -----
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc@bcm.tmc.edu

----- Project Information -----
Center Project name: TUDS
Center Clone name: CH230-2F22
----- Summary Statistics -----
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 216265 bases at least Q40
Consensus quality: 216981 bases at least Q30
Consensus quality: 217528 bases at least Q20

----- NOTE: Estimated insert size may differ from sequence length -----
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 46 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1067 1066: contig of 1066 bp in length
1067 1166: gap of unknown length

1167 2355: contig of 1189 bp in length
2356 2455: gap of unknown length
2456 3677: contig of 1222 bp in length
3678 3777: gap of unknown length
3778 5145: contig of 1368 bp in length
5146 5245: gap of unknown length
5246 6443: contig of 1198 bp in length
6444 7700: gap of unknown length
7701 7801: gap of unknown length
7802 9179: contig of 1378 bp in length
9179 9279: gap of unknown length
9279 10397: contig of 1119 bp in length
10398 10497: gap of unknown length
10498 11814: contig of 1317 bp in length
11815 11914: gap of unknown length
11915 12984: contig of 1070 bp in length
12985 13084: gap of unknown length
13085 14314: contig of 1230 bp in length
14315 14414: gap of unknown length
14415 15533: contig of 1119 bp in length
15534 15634: gap of unknown length
15634 16692: contig of 1059 bp in length
16692 16792: gap of unknown length
16793 17990: contig of 1198 bp in length
17991 18090: gap of unknown length
18091 19148: contig of 1058 bp in length
19149 19248: gap of unknown length
19249 20311: contig of 1063 bp in length
20312 20411: gap of unknown length
20412 21612: contig of 1200 bp in length
21612 21711: gap of unknown length
21712 22800: contig of 1089 bp in length
22801 22900: gap of unknown length
22901 23960: contig of 1060 bp in length
23961 24060: gap of unknown length
24061 25114: contig of 1054 bp in length
25115 25214: gap of unknown length
25215 26371: contig of 1157 bp in length
26372 26471: gap of unknown length
26472 27622: contig of 1151 bp in length
27623 27722: gap of unknown length
27723 28851: contig of 1129 bp in length
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30134 30233: gap of unknown length
30234 31500: contig of 1267 bp in length
31501 31600: gap of unknown length
31601 32790: contig of 1190 bp in length
32791 32890: gap of unknown length
32891 34072: contig of 1182 bp in length
34073 34172: gap of unknown length
34173 35173: contig of 1001 bp in length
35174 35273: gap of unknown length
35274 36350: contig of 1077 bp in length
36351 36450: gap of unknown length
36451 38017: contig of 1567 bp in length
38018 38117: gap of unknown length
38119 39244: contig of 1127 bp in length
39245 39344: gap of unknown length
39345 40695: contig of 1352 bp in length
40696 40796: gap of unknown length
40797 41966: contig of 1170 bp in length
41967 42066: gap of unknown length
42067 43527: contig of 1461 bp in length
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43629 45091: contig of 1464 bp in length
45092 45191: gap of unknown length
45192 46386: contig of 1195 bp in length
46387 46486: gap of unknown length
46487 50256: contig of 3770 bp in length
50257 50356: gap of unknown length
50357 59360: contig of 9004 bp in length

Consensus quality: 165521 bases at least Q40
 Consensus quality: 166522 bases at least Q30
 Consensus quality: 166832 bases at least Q20
 Insert size: 157000; agarose-fp
 Insert size: 167118; sum-of-ctnigs
 Quality coverage: 8.9 in Q20 bases; agarose-fp
 Quality coverage: 8.4 in Q20 bases; sum-of-ctnigs

NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1. 3475: contig of 3475 bp in length
 3476 3575: gap of 100 bp
 3576 14901: contig of 11326 bp in length
 14902 15001: gap of 100 bp
 15002 26861: contig of 11860 bp in length
 26862 26961: gap of 100 bp
 26962 46335: contig of 19374 bp in length
 46336 46435: gap of 100 bp
 46436 61029: contig of 14594 bp in length
 61030 61129: gap of 100 bp
 61130 106522: contig of 45393 bp in length
 106523 106622: gap of 100 bp
 106623 167718: contig of 61096 bp in length.

Location/Qualifiers
 1. 167718
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="RP24-511011"
 /clone_1lb="RP24-511011"
 1. 3475
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 3576. 14901
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 15002. 26861
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 26962. 46335
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 46436. 61029
 /note="assembly-fragment"
 61130. 106522
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 106623. 167718
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misc_feature 166623 167718
 misc_feature 106623 167718
 misc_feature 48745 a 32962 c 33768 g 51639 t 604 others

BASE COUNT 48745 a 32962 c 33768 g 51639 t 604 others
 ORIGIN

Alignment Scores:
 Pred. No.: 5,48e-45 Length: 167718
 Score: 673.00 Matches: 123
 Percent Similarity: 96.15% Conservative: 2
 Best Local Similarity: 94.62% Mismatches: 5
 Query Match: 45.35% Indels: 0
 DB: 2 Gaps: 0

US-09-600-932-2 (1-277) x AC115924 (1-167718)

OY 148 Val11eAaGly1eArGluThrGluGluSerPheTyrTrpIleValGlnGluGluLys 167
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 Db 76672 GTTATACAGGAGCGGAGAAACGAGAAATTCATCATTCATTCGACGAGAGAGAG 76931
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OY 168 AsnTyrArGluSerLeuThrHisCysArgIleArgGlyGlyMetLeuAlaMetProLys 187
 |||||||
 Db 76932 AACACACGAGGAATCTCGACCACTCGACGATCGAGAGGAGGATGACCATGCCCAAG 76991
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OY 188 AspGluAlaAlaAsnThrLeuIleAlaAspTyrValAlaLysSerGlyPhePheArgVal 207
 |||||||

Db 76992 GATGACAGTCGTAAACACCTTATTCGTACTATGTCGCCAAGAGTCTTCTTCAGAGTG 77051
 OY 208 Phe11eGlyVal1aAsnAplEug1uArgGluGlyTrpMetPheThrAspAsnThrPro 227
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 Db 77052 TTCATTGGGGTCAATGACCTTGAGAGGAGGGGCAATATGTCTTCACAGATTAACACTCCCA 77111
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OY 228 LeuGlnAsnTyrSerAsnTrpAsnGluGlyLysProSerAspProTyrGlyHisGluAsp 247
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 Db 77112 TTCAGAACTACACACACTGGAGAGGAGAGAACCTTGTGACCCCTCCGGCATGAGAGAC 77171
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OY 248 CysTAlaLueMetLeuSerSerGlyArgTyrPAsnAspPhrGlyCysHisLeuThrMetTyr 267
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 Db 77172 TGTGTGAGAGAGTGTGACCTCGCAGGAGTGAATGACACAGAGTGTCACTTACCATGTAT 77231
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OY 268 PheValCysGluPheIleTyrLysLys 277
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Db 77232 TTCTCTGTGAGTGTTCACAGAGAAAAA 77261
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RESULT 12
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 LOCUS Homo sapiens BAC clone RP11-568H24 from 2, complete sequence.
 ACCESSION AC010907
 VERSION AC010907.10 GI:15321567
 KEYWORDS HTG.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.

REFERENCE
 AUTHORS Du,H., Haakenson,W. and Dixon,R.
 TITLE The sequence of Homo sapiens BAC clone RP11-568H24
 JOURNAL Unpublished (2001)
 REFERENCE
 AUTHORS 3 (bases 1 to 139357)
 TITLE Waterston,R.H.
 JOURNAL Direct Submission
 Submitted (25-SEP-1999) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 4 (bases 1 to 139357)
 REFERENCE
 AUTHORS Waterston,R.H.
 TITLE Direct Submission
 Submitted (28-AUG-2001) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 5 (bases 1 to 139357)
 REFERENCE
 AUTHORS Waterston,R.
 TITLE Direct Submission
 Submitted (09-JUN-2002) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Aug 28, 2001 this sequence version replaced gi:13399437.

Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc
 Contact: sapiens@wustl.wustl.edu
 Summary Statistics
 Center project name: H_NH0568H24

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate

chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPci1 human BAC library was made from the blood of one male donor, as described by Ossewawy, K., Moon, P. Y., Zhao, B., Fiegenberg, T., Tateno, M., Catanesi, J. J. and de Jong, P. J. (1998). An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-178E6, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-568H24.

The sequence between 66093 to 66578 and 104506 to 104590 is covered only by PCR products from clone DNA, the sequence contains a dinucleotide (TG) run from 65513 to 65634 in which the exact length is unknown. The sequence contains a dinucleotide (TC) run from 104386 bp to 104631 bp in which the exact length is unknown. The sequence from base position 4458 to 6187 can not be guaranteed due to a tandem repeat.

FEATURES

Location/Qualifiers

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/map="2"  

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1340.1514  

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1611.1965  

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1973.2279  

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2324.2843  

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repeat_region 6733..7033
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OY 26 ---LeuGlyLeuAspPLeaP----- 31
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OY 32 -----SerAArgProThrlAlaValLysAlaThrHsIstHrLleSerProGlyProLys 49
Db 283 GTTGTGTGCTCCACGACAGATGAGCTTCGTGCTGATGATGAGACAGATGGAAAGAA 342
OY 50 GLYASPARSGLYLGLYSLYASPRPROGLYGLIUGLYLGLYSLYSLYSLYSLYSLYSLY 69
Db 343 GGGCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 402
OY 70 MetGlyProLys----- 73
Db 403 GAGGGCCCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 462
OY 73 ----- 73
Db 463 GAACTGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 522
OY 74 GLYLGLYSLYGLYLGLYLGLYLGLYLGLYLGLYLGLYLGLYLGLYLGLYLGLYLGLYL 93
Db 523 GGTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 582
OY 94 ILGLYLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLY 113
Db 583 TCAGGTGCATGGGTGCCCCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 642
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OY 132 AspLleSerIleAlaArgLnuLysThrSerMetLysPheValLysAsnValIleAlaGly 151
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OY 152 IleArgLnu-----ThnGluGluLysPheTrpTyrIle 162
Db 742 TACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 801
OY 163 ValGlnGluGluLysAsnTrpArgLysSerLysLeuThrHsCysArgIleArgLysMet 182
Db 802 GCAGGTGCTGAAAGTATTCGATGATGATGATGATGATGATGATGATGATGATGATG 861
OY 183 LeuAlaMetProLysAlaPrgLysAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 201
Db 862 CTGGCTCTCCCGCTCTTCAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 921
OY 202 SerGlyPhePheArgValPheIleGlyValAsnAspLysLysLysLysLysLysLys 221
Db 922 AACAGG-----CATGCTTACTGAGCATGATGATGATGATGATGATGATGATGATG 975
OY 222 PheThrAspAsnTrpProLysGlnAsnTrpSerAsnTrpAsnGluGlyLysProSerAsp 241
Db 976 TACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1032
OY 242 -----ProTyrGlyHisGluAspCysValGlyMetLysSerSerGlyLysTrpAsn 258
Db 1033 AGGGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1092
OY 259 AspThrGlyCysHisLysLeuThrMetLysPheValCysGluPhe 272
Db 1093 GACATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1134

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RESULT 14
BRLSPD BRLSPD 1454 bp mRNA linear MM 23-DEC-1993
LOCUS B.taurus mRNA for lung surfactant protein D.
DEFINITION X75911
ACCESSION X75911.1 GI:415938
VERSION
KEYWORDS lung surfactant protein D.

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SOURCE COV.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 1454)
AUTHORS Lim,B.L., Lu,J. and Reid,K.B.
TITLE Structural similarity between bovine conglutinin and bovine lung
surfactant protein D and demonstration of liver as a site of
synthesis of conglutinin
JOURNAL Immunology 78 (1), 159-165 (1993)
MEDLINE 93170856
PUBMED 8436402
REFERENCE 2 (bases 1 to 1454)
AUTHORS Lim,B.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-1993) B. Lim, MRC Immunochimistry Unit, Dept. of
Biochemistry, Univ. of Oxford, South Parks Rd., Oxford, OX1 30U, UK
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sig_peptide 162..161
mat_peptide 162..1208
poly_signal 1313..1318
BASE COUNT 365 a 383 c 452 g 254 t
ORIGIN
Alignment Scores:
Pred. No.: 2,466-20 Length: 1454
Score: 349.50 Matches: 89
Percent Similarity: 42.91% Conservative: 38
Best Local Similarity: 30.07% Mismatches: 110
Query Match: 23.55% Indels: 59
DB: 4 Gaps: 8
US-09-600-932-2 (1-277) x BRLSPD (1-1454)
OY 26 LeuGlyLeuAspPLeaP-----ProThrlAlaValLysAlaThrHsIstHrLleSer 45
Db 351 ATGGGCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 386
OY 46 ProGlyProLysGlyAspAspGlyLysGlyAspPro-----Gly 59
Db 387 CCGGAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 446
OY 60 GlnGluGlyLysHisGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 79
Db 447 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 506
OY 80 GlyAspMetGlyAspArgGlyAsnIle-----GlyLysThrGlyPro 93
Db 507 GGAGACACTGGGCGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 566
OY 94 ILGLYLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLY 102
Db 567 GCAGGTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 626

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